



2005\_0221A - HONDA - revised SEQ for filing 9-28-07  
Sequence Listing

SEQUENCE LISTING

<110> HONDA, Mitsuo  
MATSUO, Kazuhiro  
KANEKIYO, Masaru

<120> A recombinant BCG vaccine

<130> 2005-0221A/JFW/00653

<140> 10/524,586

<141> 2005-02-15

<150> JP2002-237610

<151> 2002-08-16

<160> 13

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence: Synthetic oligonucleotide

<400> 1

aatggatcct atagtcgaga acctc

25

<210> 2

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence: Synthetic oligonucleotide

<400> 2

aatgggcccct tacaaaactc ttgctttatg g

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<210> 3

<211> 706

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (5)..(700)

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile  
1 5 10 15

tcg ccg cgc acc ctg aac gcc tgg gtc aag gtc gtc gag gag aag gcc 97  
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Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala		
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Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala		
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acc	ccg	cag	gac	ctg	aac	acc	atg	ctg	aac	acc	gtc	ggc	ggc	cac	cag	193	
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln		
		50					55					60					
gcc	gcc	atg	cag	atg	ctg	aag	gag	acc	atc	aac	gag	gag	gcc	gcc	gag	241	
Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu		
	65					70					75						
tgg	gac	cgc	ctg	cac	ccg	gtc	cac	gcc	ggc	ccc	atc	gca	ccg	ggc	cag	289	
Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln		
	80					85				90					95		
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Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu		
				100					105					110			
cag	gag	cag	atc	ggc	tgg	atg	acc	cac	aac	ccg	ccg	atc	ccg	gtc	ggc	385	
Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	His	Asn	Pro	Pro	Ile	Pro	Val	Gly		
			115					120					125				
gag	atc	tac	aag	cgc	tgg	atc	atc	ctg	ggc	ctg	aac	aag	atc	gtc	cgc	433	
Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg		
		130					135					140					
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Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu		
	145					150					155						
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	160				165					170					175		
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Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val		
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cag	aac	gcc	aac	ccg	gac	tgc	aag	acc	atc	ctg	aag	gcc	ctg	ggt	ccg	625	
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro		
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Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly		
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ccg	ggc	cac	aag	gcg	cgc	gtc	ctg	taa	gggccc							706	
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<210> 4

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligopeptide

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<400> 4  
Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu  
1 5 10 15

<210> 5  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial Sequence: Synthetic oligopeptide

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<210> 6  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 6  
Met Ala Lys Thr Ile  
1 5

<210> 7  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial Sequence: Synthetic oligopeptide

<400> 7  
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<210> 8  
<211> 85  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial Sequence: Synthetic oligonucleotide

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<210> 9  
<211> 39  
<212> DNA  
<213> Artificial Sequence

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<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 9

ATGGCCAAGA CAATTGCTCG AGGGGATCCG ATCGTG CAG 39

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 10

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<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 11

CGCGTCCTGT AAGGGCCC 18

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial Sequence: Synthetic oligonucleotide

<400> 12

AGAGTTTTGT AAGGGCCC 18

<210> 13

<211> 706

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (5)..(700)

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 13

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Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile  
1 5 10 15

tca cct aga act tta aat gac tgg gta aaa gta gta gaa gag aag gtt 97  
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala

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ttc agc cca gaa gta ata ccc atg ttt tca gca tta tca gaa gga gcc	145
Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala	
35 40 45	
acc cca caa gat tta aat acc atg cta aac aca gtg ggg gga cat caa	193
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
50 55 60	
gca gcc atg caa atg tta aaa gag acc atc aat gag gaa gct gca gaa	241
Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu	
65 70 75	
tgg gat aga ttg cat cca gtg cat gca ggg cct att gca cca ggc cag	289
Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln	
80 85 90 95	
atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt	337
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu	
100 105 110	
cag gaa caa ata gga tgg atg aca cat aat cca cct atc cca gta gga	385
Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile Pro Val Gly	
115 120 125	
gaa atc tat aaa aga tgg ata atc ctg gga tta aat aaa ata gta aga	433
Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg	
130 135 140	
atg tat agc cct acc agc att ctg gac ata aga caa gga cca aag gaa	481
Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu	
145 150 155	
ccc ttt aga gac tat gta gac cga ttc tat aaa act cta aga gcc gag	529
Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu	
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caa gct tca caa gag gta aaa aat tgg atg aca gaa acc ttg ttg gtc	577
Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val	
180 185 190	
caa aat gcg aac cca gat tgt aag act att tta aaa gca ttg gga cca	625
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro	
195 200 205	
gga gcg aca cta gaa gaa atg atg aca gca tgt cag gga gtg ggg gga	673
Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly	
210 215 220	
ccc ggc cat aaa gca aga gtt ttg taa gggccc	706
Pro Gly His Lys Ala Arg Val Leu	
225 230	